## GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2006, 09:26:06; Search time 0.001 Seconds

(without alignments)

143.112 Million cell updates/sec

Title: us-10-088-666-1

Perfect score: 267

Sequence: 1 tatatggaagtaagaccct.....agtagttgggggatcqccc 267

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 13 segs, 268 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : rgedb1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

ult No.	· Score	Query Match	Length	DB	ID	Description
1	25	9.4	25	1	AX105801	ACCESSION: AX105801
2	25	9.4	25	1	AX105830	ACCESSION: AX105830
3	23	8.6	23	1	AX105781	ACCESSION: AX105781
4	21	7.9	21	1	AX105749	ACCESSION: AX105749
5	21	7.9	21	1	AX105827	ACCESSION: AX105827
6	20	7.5	20	1	AR105913	ACCESSION: AR105913
7	20	7.5	20	1	E04248	ACCESSION: E04248
8	20	7.5	20	1	E07340	ACCESSION: E07340
9	20	7.5	20	1	E07586	ACCESSION: E07586
10	20	7.5	20	1	AX105802	ACCESSION: AX105802
11	20	7.5	. 20	1	AX105826	ACCESSION: AX105826
12	18	6.7	18	1	AX105791	ACCESSION: AX105791
13	15	5.6	15	1	AR371336	ACCESSION: AR371336
14	11	4.1	21	1	AX105749	ACCESSION: AX105749
15	8.2	3.1	25	1	AX105801	ACCESSION: AX105801
16	7.8	2.9	25	1	AX105830	ACCESSION: AX105830
17	7.4	2.8	20	1	AX105802	ACCESSION: AX105802
	No. 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	No. Score  1 25 2 25 3 23 4 21 5 21 6 20 7 20 8 20 9 20 10 20 11 20 11 20 12 18 13 15 14 11 15 8.2 16 7.8	No. Score Match  1 25 9.4 2 25 9.4 3 23 8.6 4 21 7.9 5 21 7.9 6 20 7.5 7 20 7.5 8 20 7.5 9 20 7.5 10 20 7.5 11 20 7.5 11 20 7.5 12 18 6.7 13 15 5.6 14 11 4.1 15 8.2 3.1 16 7.8 2.9	No. Score Match Length  1 25 9.4 25 2 25 9.4 25 3 23 8.6 23 4 21 7.9 21 5 21 7.9 21 6 20 7.5 20 7 20 7.5 20 8 20 7.5 20 9 20 7.5 20 9 20 7.5 20 10 20 7.5 20 11 20 7.5 20 11 20 7.5 20 12 18 6.7 18 13 15 5.6 15 14 11 4.1 21 15 8.2 3.1 25 16 7.8 2.9 25	No. Score Match Length DB  1 25 9.4 25 1 2 25 9.4 25 1 3 23 8.6 23 1 4 21 7.9 21 1 5 21 7.9 21 1 6 20 7.5 20 1 7 20 7.5 20 1 8 20 7.5 20 1 9 20 7.5 20 1 10 20 7.5 20 1 11 20 7.5 20 1 11 20 7.5 20 1 11 20 7.5 20 1 11 21 18 6.7 18 1 13 15 5.6 15 1 14 11 4.1 21 1 15 8.2 3.1 25 1 16 7.8 2.9 25 1	No. Score Match Length DB ID  1 25 9.4 25 1 AX105801 2 25 9.4 25 1 AX105830 3 23 8.6 23 1 AX105781 4 21 7.9 21 1 AX105749 5 21 7.9 21 1 AX105827 6 20 7.5 20 1 AR105913 7 20 7.5 20 1 E04248 8 20 7.5 20 1 E07340 9 20 7.5 20 1 E07586 10 20 7.5 20 1 E07586 10 20 7.5 20 1 AX105802 11 20 7.5 20 1 AX105802 11 20 7.5 20 1 AX105826 12 18 6.7 18 1 AX105791 13 15 5.6 15 1 AR371336 14 11 4.1 21 1 AX105749 15 8.2 3.1 25 1 AX105801 16 7.8 2.9 25 1 AX105830

С	18	7.2	2.7	20	1	AR105913	ACCESSION: AR105913
С	19	7.2	2.7	20	1	E04248	ACCESSION: E04248
С	20	7.2	2.7	20	1	E07340	ACCESSION: E07340
С	21	7.2	2.7	20	1	E07586	ACCESSION: E07586
С	22	7.2	2.7	21	1	AX105827	ACCESSION: AX105827
	23	6.8	2.5	23	1	AX105781	ACCESSION: AX105781
	24	6.2	2.3	15	1	AR371336	ACCESSION: AR371336
	25	6	2.2	18	1	AX105791	ACCESSION: AX105791
С	26	5.8	2.2	20	1	AX105826	ACCESSION: AX105826

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## GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: October 12, 2006, 09:28:05; Search time 0.001 Seconds

(without alignments)

106.800 Million cell updates/sec

Title: us-10-088-666-1

Perfect score: 267

Sequence: 1 tatatggaagtaagacccct.....agtagttgggggatcgcccc 267

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 8 seqs, 200 residues

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Q

Maximum Match 100%

Listing first 300 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

			ð					
Resi	ult		Query					
1	No.	Score	Match	Length	DB	ID	Description	on
	1	25	9.4	25	1	US-11-348-413-350688	Sequence	350688,
	2	25	9.4	25	1	US-11-348-413-350689	Sequence	350689,
	3	25	9.4	25	1	US-11-348-413-988351	Sequence	988351,
	4	25	9.4	25	1	US-11-348-413-988352	Sequence	988352,
	5	25	9.4	25	1	US-11-348-413-988353	Sequence	988353,
	6	25	9.4	25	1	US-11-348-413-988354	Sequence	988354,
	7	25	9.4	25	1	US-11-348-413-988355	Sequence	
	8	25	9.4	25	1	US-11-348-413-988356	Sequence	
С	9	· 6.6	2.5	25	1	US-11-348-413-350688	Sequence	350688,
С	10	6.6	2.5	25	1	US-11-348-413-350689	Sequence	350689,
С	11	6.6	2.5	25	1	US-11-348-413-988352	Sequence	988352,
С	12	6.6	2.5	25	1	US-11-348-413-988353	Sequence	988353,
С	13	6.6	2.5	25	1	US-11-348-413-988354	Sequence	988354,
C	14	6.6	2.5	25	1	US-11-348-413-988355	Sequence	988355,
С	15	6.6	2.5	25	1	US-11-348-413-988356	Sequence	•
С	16	6.2	2.3	25	1	US-11-348-413-988351	Sequence	

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OM nucleic - nucleic search, using sw model

Run on: October 12, 2006, 09:27:26; Search time 0.001 Seconds

(without alignments)

18.690 Million cell updates/sec

Title: us-10-088-666-1

Perfect score: 267

Sequence: 1 tatatggaagtaagacccct....agtagttgggggatcgcccc 267

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 35 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Res	ult No.	Score	Query Match	Length	DB	ID	Description
	1	20	7.5	20	1	US-08-944-974A-1	Sequence 1, Appli
С	2	15	5.6	15	1	US-08-461-210-30	Sequence 30, Appl
С	3	7.2	2.7	20	1	US-08-944-974A-1	Sequence 1, Appli
	4	6.2	2.3	15	1	US-08-461-210-30	Sequence 30. Appl